

GenCore version 5.1.7  
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OM nucleic - nucleic search, using sw model

Run on: April 1, 2006, 04:15:51 ; Search time 2046 Seconds  
(without alignments)

2361.531 Million cell updates/sec

Title: US-10-767-609-1

Perfect score: 85

Sequence: 1 gtgagtgtgttagttc.....gcacctatttcatttcag 85

Scoring table: IDENTITY NUC

Gapop 10.0 , Gapext 1.0

Searched: 5883141 seqs, 28421725653 residues

Total number of hits satisfying chosen parameters: 11766282

Minimum DB seq length: 0

Maximum DB seq length: 2000000000

Post-processing: Minimum Match 0%

Maximum Match 100%

Listing first 45 summaries

Database :

GenEmbl.\*

1: gb\_ba.\*

2: gb\_in.\*

3: gb\_env.\*

4: gb\_on.\*

5: gb\_ov.\*

6: gb\_pat.\*

7: gb\_ph.\*

8: gb\_pr.\*

9: gb\_ro.\*

10: gb\_sts.\*

11: gb\_ey.\*

12: gb\_un.\*

13: gb\_vi.\*

14: gb\_htg.\*

15: gb\_pl.\*

Pred. No. is the number of results predicted by chance to have a score greater than or equal to the score of the result being printed, and is derived by analysis of the total score distribution.

#### SUMMARIES

Result No.	Score	Query Match	Length	DB ID	Description
1	85	100.0	85	6 AX025268	AX025268 Sequence
2	85	100.0	103	1 S74256	S74256 rola-transf
3	85	100.0	700	15 X76001	X76001 A.thaliana
4	85	100.0	720	1 AR001A	X12579 Agrobacteri
5	85	100.0	831	11 AF442734	AF442734 Synthetic
6	85	100.0	831	11 AF442735	AF442735 Synthetic
7	85	100.0	21126	1 RIATL	K03313 Integrated
8	85	100.0	21126	6 AR050120	AR050120 Sequence
9	85	100.0	21126	6 IO4770	IO4770 Sequence 94
10	85	100.0	21126	6 I24453	I24453 Sequence 19
11	77	90.6	86	6 AX078800	AX078800 Sequence
12	35.8	42.1	167978	8 AC096914	AC096914 Homo sapi
13	35.8	42.1	193384	14 AC021057	AC021057 Homo sapi
14	35.8	42.1	275519	14 AC119596	AC119596 Rattus no
15	35.6	41.9	141016	14 AC148204	AC148204 Callicebu
16	35.6	41.9	179882	14 AC159168	AC159168 Callicebu
17	34.2	40.2	236039	14 AC121212	AC121212 Rattus no
18	34	40.0	105707	5 BX950225	BX950225 Zebrafish

c 19 33.8 39.8 188633 9 AC159301  
 c 20 33.4 39.3 110000 15 CR382134\_09  
 c 21 33.4 39.3 110000 15 CR382134\_10  
 c 22 33.4 39.3 174655 8 AC023347  
 c 23 33.4 39.3 246322 14 AC133966  
 c 24 33 38.8 1407 6 AX416421  
 c 25 33 38.8 187145 14 CR626902  
 c 26 33 38.8 290683 1 AE017329  
 c 27 33 38.8 295050 1 AL591982  
 c 28 33 38.8 349980 6 AX641671  
 c 29 32.8 38.6 116909 15 AC157349  
 c 30 32.4 38.1 153106 14 AC162469  
 c 31 32.4 38.1 170456 14 AC144751  
 c 32 32.4 38.1 203456 14 AC144999  
 c 33 32.4 38.1 337101 8 HSKSRPXR  
 c 34 32.4 38.1 349980 6 AX344555  
 c 35 32.2 37.9 78245 5 BX950855  
 c 36 32.2 37.9 161001 8 AC068775  
 c 37 32.2 37.9 188938 14 AC119064  
 c 38 32.2 37.9 199551 14 AC006281  
 c 39 32.2 37.9 218834 14 AC105640  
 c 40 32.2 37.9 226994 14 AC128720  
 c 41 32.2 37.9 251551 2 AE014844  
 c 42 32.2 37.9 319223 14 AC128879  
 c 43 32 37.6 659 10 BV253440  
 c 44 32 37.6 6031 6 AX323720  
 c 45 32 37.6 125987 15 CT009553

#### ALIGNMENTS

RESULT 1  
 AX025268  
 LOCUS AX025268 85 bp DNA linear PAT 16-SEP-2000  
 DEFINITION Sequence 1 from Patent EP1002868.  
 ACCESSION AX025268  
 VERSION AX025268.1 GI:10186982  
 KEYWORDS  
 SOURCE Agrobacterium rhizogenes (Rhizobium rhizogenes)  
 ORGANISM Agrobacterium rhizogenes  
 Bacteria; Proteobacteria; Alphaproteobacteria; Rhizobiales;  
 Rhizobiaceae; Agrobacterium.

REFERENCE 1  
 AUTHORS Defez, R. and Spena, A.  
 TITLE Method to control gene expression in bacteria namely rhizobiaceae to improve root nodule development nitrogen fixation and plant biomass production  
 JOURNAL Patent: EP 1002868-A 1 24-MAY-2000;  
 CONSIGLIO NAZIONALE RICERCA (IT) ; G IN E ST R A SOCIETA CONSORTI (IT)

FEATURES  
 source Location/Qualifiers  
 1..85  
 /organism="Agrobacterium rhizogenes"  
 /mol\_type="unassigned DNA"  
 /db\_xref="taxon:359"

#### ORIGIN

Query Match 100.0%; Score 85; DB 6; Length 85;  
 Best Local Similarity 100.0%; Pred. No. 7.3e-09;  
 Matches 85; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

Qy 1 GTGAGTGTGTTGAGTTCAATTATTTTCAAGCTGTGTTTCCCTTTTCT 60  
 |||||  
 Db 1 GTGAGTGTGTTGAGTTCAATTATTTTCAAGCTGTGTTTCCCTTTTCT 60  
 |||||  
 Qy 61 AATATGCACCTATTTCATGTTTCAG 85  
 |||||  
 Db 61 AATATGCACCTATTTCATGTTTCAG 85

RESULT 2  
 S74256